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OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/731,816DATE: 12/26/2000
TIME: 15:15:28Input Set : A:\PF470P1.ST25.txt
Output Set: N:\CRF3\12262000\I731816.raw

P5

ENTERED

3 <110> APPLICANT: Ebner, Reinhard
4 Ruben, Steven
6 <120> TITLE OF INVENTION: Interleukins-21 and 22
8 <130> FILE REFERENCE: PF470P1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/731,816
C--> 10 <141> CURRENT FILING DATE: 2000-12-08
10 <150> PRIOR APPLICATION NUMBER: 60/169,837
11 <151> PRIOR FILING DATE: 1999-12-09
13 <150> PRIOR APPLICATION NUMBER: 09/320,713
14 <151> PRIOR FILING DATE: 1999-05-27
16 <150> PRIOR APPLICATION NUMBER: 60/087,340
17 <151> PRIOR FILING DATE: 1998-05-29
19 <150> PRIOR APPLICATION NUMBER: 60/099,805
20 <151> PRIOR FILING DATE: 1998-09-10
22 <150> PRIOR APPLICATION NUMBER: 60/131,965
23 <151> PRIOR FILING DATE: 1999-04-30
25 <150> PRIOR APPLICATION NUMBER: PCT US99/11644
26 <151> PRIOR FILING DATE: 1999-05-27
28 <160> NUMBER OF SEQ ID NOS: 32
30 <170> SOFTWARE: PatentIn version 3.0
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 705
34 <212> TYPE: DNA
35 <213> ORGANISM: HOMO SAPIENS
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (2)..(262)
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42 g gca cga gtg gac acg gat gag gac cgc tat cca cag aag ctg gcc ttc 49
43 Ala Arg Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe
44 1 5 10 15
46 gcc gag tgc ctg tgc aga ggc tgt atc gat gca cgg acg ggc cgc gag 97
47 Ala Glu Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu
48 20 25 30
50 aca gct gcg ctc aac tcc gtg cgg ctg ctc cag agc ctg ctg gtg ctg 145
51 Thr Ala Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu
52 35 40 45
54 cgc cgc cgg ccc tgc tcc cgc gac ggc tgg ggg ctc ccc aca cct ggg 193
55 Arg Arg Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly
56 50 55 60
58 gcc ttt gcc ttc cac acc gag ttc atc cac gtc ccc gtc gcc tgc acc 241
59 Ala Phe Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr
60 65 70 75 80
62 tgc gtg ctg ccc cgt tca tlg tgaccgccaa ggcggtgggg cccttagact 292
63 Cys Val Leu Pro Arg Ser Val
64 85
66 ggacaagtggt gctccccaga gggcaccccc tatttatgtg tatttattgt tatttatatg 352

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68 cctcccccaa cactaccctt ggggtctggg cattccccgt gtctggagga cagcccccca 412
70 ctgttctect catctccagc ctcagtagtt gggggtwga ggagctcagc acctcttcca 472
72 gcccttaaaq ctgcagaaaa ggtgtcacac ggtgcctgt accttgggtc cctgtcctgc 532
74 tcccggtctc ccttacccta tcaactggct caggcccccg caggctgcct cttcccaacc 592
76 tcccttggag taccctgttt tcttaaacaa ttatttaagt gtacgtgtat tattaaactg 652
78 atgaacacaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 705
81 <210> SEQ ID NO: 2
82 <211> LENGTH: 87
83 <212> TYPE: PRT
84 <213> ORGANISM: HOMO SAPIENS
86 <400> SEQUENCE: 2
88 Ala Arg Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe
89 1 5 10 15
92 Ala Glu Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu
93 20 25 30
96 Thr Ala Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu
97 35 40 45
100 Arg Arg Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly
101 50 55 60
104 Ala Phe Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr
105 65 70 75 80
108 Cys Val Leu Pro Arg Ser Val
109 85
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 1641
114 <212> TYPE: DNA
115 <213> ORGANISM: HOMO SAPIENS
117 <220> FEATURE:
118 <221> NAME/KEY: CDS
119 <222> LOCATION: (3)..(482)
121 <400> SEQUENCE: 3
122 gg aat tcg gca cga gct cgt gcc gtg etc agt gcc ttc cac cac acg 47
123 Asn Ser Ala Arg Ala Arg Ala Val Leu Ser Ala Phe His His Thr
124 1 5 10 15
126 ctg cag ctg ggg ccg cgt gag cag gcg cgc aac gcg agc tgc ccg gca 95
127 Leu Gln Leu Gly Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala
128 20 25 30
130 ggg ggc agg ccc gcc gac cgc cgc ttc cgg ccg ccc acc aac ctg cgc 143
131 Gly Gly Arg Pro Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg
132 35 40 45
134 agc gtg tgc ccc tgg gcc tac aga atc tcc tac gac ccg gcg agg tac 191
135 Ser Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr
136 50 55 60
138 ccc agg tac ctg cct gaa gcc tac tgc ctg tgc cgg ggc tgc ctg acc 239
139 Pro Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr
140 65 70 75
142 ggg ctg ttc ggc gag gag gac gtg cgc ttc cgc agc gcc cct gtc tac 287
143 Gly Leu Phe Gly Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr
144 80 85 90 95

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146 atg ccc acc gtc gtc ctg cgc cgc acc ccc gcc tgc gcc gcc gcc cgt      335
147 Met Pro Thr Val Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg
148      100      105      110
150 tcc gtc tac acc gag gcc tac gtc acc atc ccc gtg gcc tgc acc tgc      383
151 Ser Val Tyr Thr Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys
152      115      120      125
154 gtc ccc gag ccg gag aag gac gca gac agc atc aac tcc agc atc gac      431
155 Val Pro Glu Pro Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp
156      130      135      140
158 aaa cag gcc gcc aag ctc ctg ggc ccc aac gac gcg ccc gct gcc      479
159 Lys Gln Gly Ala Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly
160      145      150      155
162 ccc tgaggccggg cctgccccgg gaggtctccc cggcccgcat cccgagggcg      532
163 Pro
164 160
166 ccaagctgga gccgcctgga gggetcggtc ggcgaacctet gaagagagtg caccgagcaa      592
168 accaagtgcc ggagcaccag cgcgcctttt ccatggagac tcgtaagcag cttcatctga      652
170 cccgggcatc cctggcttgc ttttagctac aagcaagcag cgtggctgga agctgaggg      712
172 aaacgaccgc gccacggcat cctgtgtgcg gcccgcatgg aggggtttgga aaagtccacg      772
174 gaggtccctt gagggacctc tcagatcggc tgctgcgggt gccgggcgtg actcaccgct      832
176 ggggtgcttg caaagagata gggacgcata tgctttttaa agcaatctaa aaataataat      892
178 aagtatagcg actatatacc tactttttaaa atcaactggt ttgaatagag gcagagctat      952
180 tttatattat caaatgagag ctactctggt acatttctta acatataaac atcgttttta      1012
182 cttcttcttg tagaattttt taaagcataa ttggaatcct tggataaaatt ttgtagctgg      1072
184 tacactctgg cctgggtctc tgaattcaag ctgtcaccga tggctgactg atgaaatgga      1132
186 cagctctcat ctgacccaact cttccttcca ctgaaggtct tcacgggacct ccaggtggac      1192
188 caaagggatg cacagcgagg tcgcatgccc cagggccagc taagagttcc aaaqatctca      1252
190 gatttggttt tagtcatyaa tacataaaca gtctcaaaat cgcacaattt tttccccctt      1312
192 ttgaaagcca ctggggccaa tttgtggtta agaggtggtg agataagaag tggaaagtga      1372
194 catctttgcc agttgtcaga agaattccaag caggtattgg cttagtgtga agggctttag      1432
196 gatcaggctg aatatgagga caaagtgggc caggttagca tctgcagaga tcaatctgga      1492
198 ggcttctgtt tctgcattct gccacgagag ctgagtcctt gatcttttct ttagattgaa      1552
200 agtctgtctc tgaacacaat tatttgtaaa agttaytagt tcttttttaa atcattaaaa      1612
202 gaggttgctt gaaaaaaaaa aaaaaaaaaa
205 <210> SEQ ID NO: 4
206 <211> LENGTH: 160
207 <212> TYPE: PRT
208 <213> ORGANISM: HOMO SAPIENS
210 <400> SEQUENCE: 4
212 Asn Ser Ala Arg Ala Arg Ala Val Leu Ser Ala Phe His His Thr Leu
213 1      5      10      15
216 Glu Leu Gly Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly
217      20      25      30
220 Gly Arg Pro Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser
221      35      40      45
224 Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro
225      50      55      60
228 Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly
229 65      70      75      80

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232 Leu Phe Gly Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met
233                               85                      90          95
236 Pro Thr Val Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser
237                               100                     105         110
240 Val Tyr Thr Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val
241                               115                     120         125
244 Pro Glu Pro Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys
245                               130                     135         140
248 Gln Gly Ala Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
249 145                               150                     155         160
252 <210> SEQ ID NO: 5
253 <211> LENGTH: 155
254 <212> TYPE: PRT
255 <213> ORGANISM: HOMO SAPIENS
257 <400> SEQUENCE: 5
259 Met Thr Pro Gly Lys Thr Ser Leu Val Ser Leu Leu Leu Leu Ser
260 1                               5                      10          15
262 Leu Glu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly
263                               20                      25          30
265 Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn
266                               35                      40          45
268 Leu Asn Ile His Asn Arg Asn Thr Asn Pro Lys Arg Ser Ser
269 50                               55                      60
271 Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
272 65                               70                      75          80
274 Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
275                               85                      90          95
277 Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
278                               100                     105         110
280 Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His
281                               115                     120         125
283 Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
284 130                               135                     140
286 Thr Cys Val Thr Pro Ile Val His His Val Ala
287 145                               150                     155
289 <210> SEQ ID NO: 6
290 <211> LENGTH: 158
291 <212> TYPE: PRT
292 <213> ORGANISM: MUS MUSCULUS
294 <400> SEQUENCE: 6
296 Met Ser Pro Gly Arg Ala Ser Ser Val Ser Leu Met Leu Leu Leu
297 1                               5                      10          15
299 Leu Ser Leu Ala Ala Thr Val Lys Ala Ala Ala Ile Ile Pro Gln Ser
300                               20                      25          30
302 Ser Ala Cys Pro Asn Thr Glu Ala Lys Asp Phe Leu Gln Asn Val Lys
303                               35                      40          45
305 Val Asn Leu Lys Val Phe Asn Ser Leu Gly Ala Lys Val Ser Ser Arg
306 50                               55                      60
308 Arg Pro Ser Asp Tyr Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu His

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309 65          70          75          80
311 Arg Asn Glu Asp Pro Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln
312          85          90          95
314 Cys Arg His Gln Arg Cys Val Asn Ala Glu Gly Lys Leu Asp His His
315          100         105         110
317 Met Asn Ser Val Leu Ile Gln Gln Glu Ile Leu Val Leu Lys Arg Glu
318          115         120         125
320 Pro Glu Ser Cys Pro Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly
321          130         135         140
323 Val Gly Cys Thr Cys Val Ala Ser Ile Val Arg Gln Ala Ala
324 145          150          155
326 <210> SEQ ID NO: 7
327 <211> LENGTH: 151
328 <212> TYPE: PRT
329 <213> ORGANISM: VIRAL
331 <400> SEQUENCE: 7
333 Met Thr Phe Arg Met Thr Ser Leu Val Leu Leu Leu Leu Ser Ile
334 1          5          10          15
336 Asp Cys Ile Val Lys Ser Glu Ile Thr Ser Ala Gln Thr Pro Arg Cys
337          20          25          30
339 Leu Ala Ala Asn Asn Ser Phe Pro Arg Ser Val Met Val Thr Leu Ser
340          35          40          45
342 Ile Arg Asn Trp Asn Thr Ser Ser Lys Arg Ala Ser Asp Tyr Tyr Asn
343          50          55          60
345 Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu Asp Gln Asp Arg
346 65          70          75          80
348 Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr Leu Gly Cys Val
349          85          90          95
351 Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln
352          100         105         110
354 Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro Cys Pro Asn Ser
355          115         120         125
357 Phe Arg Leu Glu Lys Met Leu Val Thr Val Gly Cys Thr Cys Val Thr
358          130         135         140
360 Pro Ile Val His Asn Val Asp
361 145          150
363 <210> SEQ ID NO: 8
364 <211> LENGTH: 180
365 <212> TYPE: PRT
366 <213> ORGANISM: HOMO SAPIENS
368 <400> SEQUENCE: 8
370 Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile Phe
371 1          5          10          15
373 Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln
374          20          25          30
376 Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp
377          35          40          45
379 Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg
380          50          55          60

```

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/731,816

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:982 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:984 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:988 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:992 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:996 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:998 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
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L:1090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1092 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30